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RAW SEQUENCE LISTING   DATE: 10/30/2002 ₽ ૬
PATENT APPLICATION: US/10/086,814   TIME: 13:57:57

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

```
 3 <110> APPLICANT: Dragic, Tatjana
 4        Olson, Wlliam C.
 6 <120> TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
 8 <130> FILE REFERENCE: 61010-AB-1
10 <140> CURRENT APPLICATION NUMBER: US 10/086,814
11 <141> CURRENT FILING DATE: 2002-02-28
13 <160> NUMBER OF SEQ ID NOS: 38
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 352
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
24 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
25 1               5                   10                  15
28 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
29             20                  25                  30
32 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
33         35                  40                  45
36 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
37     50                  55                  60
40 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
41 65                  70                  75                  80
44 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
45             85                  90                  95
48 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
49             100                 105                 110
52 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
53         115                 120                 125
56 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
57     130                 135                 140
60 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
61 145                 150                 155                 160
64 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
65             165                 170                 175
68 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
69             180                 185                 190
72 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
73         195                 200                 205
76 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
77     210                 215                 220
80 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
81 225                 230                 235                 240
```

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```
 84 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
 85             245             250             255
 88 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
 89             260             265             270
 92 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
 93             275         .   280             285
 96 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
 97     290             295             300
100 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
101 305             310             315             320
104 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
105             325             330             335
108 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
109             340             345             350
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 1376
114 <212> TYPE: DNA
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 2
118 gaattccccc aacagagcca agctctccat ctagtggaca gggaagctag cagcaaacct      60
120 tcccttcact acaaaacttc attgcttggc caaaaagaga gttaattcaa tgtagacatc     120
122 tatgtaggca attaaaaacc tattgatgta taaaacagtt tgcattcatg gagggcaact     180
124 aaatacattc taggacttta taaaagatca cttttattt atgcacaggg tggaacaaga      240
126 tggattatca agtgtcaagt ccaatctatg acatcaatta ttatacatcg gagccctgcc     300
128 aaaaaatcaa tgtgaagcaa atcgcagccc gcctcctgcc tccgctctac tcactggtgt     360
130 tcatctttgg ttttgtgggc aacatgctgg tcatcctcat cctgataaac tgcaaaaggc     420
132 tgaagagcat gactgacatc tacctgctca acctggccat ctctgacctg tttttccttc     480
134 ttactgtccc cttctgggct cactatgctg ccgcccagtg ggactttgga aatacaatgt     540
136 gtcaactctt gacagggctc tattttatag gcttcttctc tggaatcttc ttcatcatcc     600
138 tcctgacaat cgataggtac ctggctgtcg tccatgctgt gtttgcttta aaagccagga     660
140 cggtcacctt tggggtggtg acaagtgtga tcacttgggt ggtggctgtg tttgcgtctc     720
142 tcccaggaat catctttacc agatctcaaa aagaaggtct tcattacacc tgcagctctc     780
144 attttccata cagtcagtat caattctgga agaatttcca gacattaaag atagtcatct     840
146 tggggctggt cctgccgctg cttgtcatgg tcatctgcta ctcgggaatc ctaaaaactc     900
148 tgcttcggtg tcgaaatgag aagaagaggc acagggctgt gaggcttatc ttcaccatca     960
150 tgattgttta ttttctcttc tgggctccct acaacattgt ccttctcctg aacaccttcc    1020
152 aggaattctt tggcctgaat aattgcagta gctctaacag gttggaccaa gctatgcagg    1080
154 tgacagagac tcttgggatg acgcactgct gcatcaaccc catcatctat gcctttgtcg    1140
156 gggagaagtt cagaaactac ctcttagtct tcttccaaaa gcacattgcc aaacgcttct    1200
158 gcaaatgctg ttctattttc cagcaagagg ctcccgagcg agcaagctca gtttacaccc    1260
160 gatccactgg ggagcaggaa atatctgtgg gcttgtgaca cggactcaag tgggctggtg    1320
162 acccagtcag agttgtgcac atggcttagt tttcatacac agcctgggct ggggggt      1376
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 12
167 <212> TYPE: PRT
168 <213> ORGANISM: Homo sapiens
170 <220> FEATURE:
171 <221> NAME/KEY: MISC_FEATURE
172 <222> LOCATION: (1)..(1)
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RAW SEQUENCE LISTING   DATE: 10/30/2002
PATENT APPLICATION: US/10/086,814   TIME: 13:57:57

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

173 <223> OTHER INFORMATION: Any amino acid
176 <220> FEATURE:
177 <221> NAME/KEY: MISC_FEATURE
178 <222> LOCATION: (2)..(2)
179 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
more t
180   han 2 amino acids, they have a sequence identical to the sequence
181   set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
182   nd extending therefrom in the amino terminal direction.
185 <220> FEATURE:
186 <221> NAME/KEY: MOD_RES
187 <222> LOCATION: (3)..(3)
188 <223> OTHER INFORMATION: SULFATATION
191 <220> FEATURE:
192 <221> NAME/KEY: MOD_RES
193 <222> LOCATION: (7)..(7)
194 <223> OTHER INFORMATION: SULFATATION
197 <220> FEATURE:
198 <221> NAME/KEY: MISC_FEATURE
199 <222> LOCATION: (11)..(11)
200 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
more
201   than 2 amino acids, they have a sequence identical to the sequenc
202   e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
203   and extending therefrom in the carboxy terminal direction.
206 <220> FEATURE:
207 <221> NAME/KEY: MISC_FEATURE
208 <222> LOCATION: (12)..(12)
209 <223> OTHER INFORMATION: Any amino acid
212 <400> SEQUENCE: 3
W--> 214 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
215 1   5   10
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 12
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
223 <220> FEATURE:
224 <221> NAME/KEY: MISC_FEATURE
225 <222> LOCATION: (2)..(2)
226 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
more t
227   han 2 amino acids, they have a sequence identical to the sequence
228   set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
229   nd extending therefrom in the amino terminal direction.
232 <220> FEATURE:
233 <221> NAME/KEY: MISC_FEATURE
234 <222> LOCATION: (1)..(1)
235 <223> OTHER INFORMATION: Xaa is any amino acid
238 <220> FEATURE:
239 <221> NAME/KEY: MOD_RES
240 <222> LOCATION: (7)..(8)
241 <223> OTHER INFORMATION: SULFATATION

RAW SEQUENCE LISTING   DATE: 10/30/2002
PATENT APPLICATION: US/10/086,814   TIME: 13:57:57

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

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       244 <220> FEATURE:
       245 <221> NAME/KEY: MISC_FEATURE
       246 <222> LOCATION: (11)..(11)
       247 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
more
       248       than 2 amino acids, they have a sequence identical to the sequenc
       249       e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
       250       and extending therefrom in the carboxy terminal direction.
       253 <220> FEATURE:
       254 <221> NAME/KEY: MISC_FEATURE
       255 <222> LOCATION: (12)..(12)
       256 <223> OTHER INFORMATION: Xaa is any amino acid
       259 <400> SEQUENCE: 4
W--> 261 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
       262 1               5                   10
       265 <210> SEQ ID NO: 5
       266 <211> LENGTH: 12
       267 <212> TYPE: PRT
       268 <213> ORGANISM: Homo sapiens
       270 <220> FEATURE:
       271 <221> NAME/KEY: MISC_FEATURE
       272 <222> LOCATION: (1)..(1)
       273 <223> OTHER INFORMATION: Xaa is any amino acid
       276 <220> FEATURE:
       277 <221> NAME/KEY: MISC_FEATURE
       278 <222> LOCATION: (2)..(2)
       279 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
more t
       280       han 2 amino acids, they have a sequence identical to the sequence
       281       set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
       282       nd extending therefrom in the amino terminal direction.
       285 <220> FEATURE:
       286 <221> NAME/KEY: MOD_RES
       287 <222> LOCATION: (3)..(3)
       288 <223> OTHER INFORMATION: SULFATATION
       291 <220> FEATURE:
       292 <221> NAME/KEY: MOD_RES
       293 <222> LOCATION: (8)..(8)
       294 <223> OTHER INFORMATION: SULFATATION
       297 <220> FEATURE:
       298 <221> NAME/KEY: MISC_FEATURE
       299 <222> LOCATION: (11)..(11)
       300 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
more
       301       than 2 amino acids, they have a sequence identical to the sequenc
       302       e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
       303       and extending therefrom in the carboxy terminal direction.
       306 <220> FEATURE:
       307 <221> NAME/KEY: MISC_FEATURE
       308 <222> LOCATION: (12)..(12)
       309 <223> OTHER INFORMATION: Xaa is any amino acid
       312 <400> SEQUENCE: 5
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RAW SEQUENCE LISTING   DATE: 10/30/2002
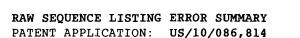PATENT APPLICATION: US/10/086,814   TIME: 13:57:57

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

W--> 314 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
     315 1   5   10
     318 <210> SEQ ID NO: 6
     319 <211> LENGTH: 12
     320 <212> TYPE: PRT
     321 <213> ORGANISM: Homo sapiens
     323 <220> FEATURE:
     324 <221> NAME/KEY: MISC_FEATURE
     325 <222> LOCATION: (1)..(1)
     326 <223> OTHER INFORMATION: Xaa is any amino acid
     329 <220> FEATURE:
     330 <221> NAME/KEY: MOD_RES
     331 <222> LOCATION: (1)..(1)
     332 <223> OTHER INFORMATION: ACETYLATION
     335 <220> FEATURE:
     336 <221> NAME/KEY: MISC_FEATURE
     337 <222> LOCATION: (2)..(2)
     338 <223> OTHER INFORMATION: Xaa represents from 0 to 9 amino acids, where if there are
more t
     339   han 2 amino acids, they have a sequence identical to the sequence
     340   set forth in SEQ ID NO: 1 beginning with the Ile at position 9 a
     341   nd extending therefrom in the amino terminal direction.
     344 <220> FEATURE:
     345 <221> NAME/KEY: MOD_RES
     346 <222> LOCATION: (3)..(3)
     347 <223> OTHER INFORMATION: SULFATATION
     350 <220> FEATURE:
     351 <221> NAME/KEY: MOD_RES
     352 <222> LOCATION: (7)..(7)
     353 <223> OTHER INFORMATION: SULFATATION
     356 <220> FEATURE:
     357 <221> NAME/KEY: MISC_FEATURE
     358 <222> LOCATION: (11)..(11)
     359 <223> OTHER INFORMATION: Xaa represents from 0 to 14 amino acids, where if there are
more
     360   than 2 amino acids, they have a sequence identical to the sequenc
     361   e set forth in SEQ ID NO: 1 beginning with the Glu at position 18
     362   and extending therefrom in the carboxy terminal direction.
     365 <220> FEATURE:
     366 <221> NAME/KEY: MISC_FEATURE
     367 <222> LOCATION: (12)..(12)
     368 <223> OTHER INFORMATION: Xaa is any amino acid
     371 <400> SEQUENCE: 6
W--> 373 Xaa Xaa Tyr Asp Ile Asn Tyr Tyr Thr Ser Xaa Xaa
     374 1   5   10
     377 <210> SEQ ID NO: 7
     378 <211> LENGTH: 12
     379 <212> TYPE: PRT
     380 <213> ORGANISM: Homo sapiens
     382 <220> FEATURE:
     383 <221> NAME/KEY: MISC_FEATURE

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/30/2002
PATENT APPLICATION: US/10/086,814   TIME: 13:57:58

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:3;  Xaa Pos. 1,2,11,12
Seq#:4;  Xaa Pos. 1,2,11,12
Seq#:5;  Xaa Pos. 1,2,11,12
Seq#:6;  Xaa Pos. 1,2,11,12
Seq#:7;  Xaa Pos. 1,2,11,12
Seq#:8;  Xaa Pos. 1,2,11,12
Seq#:9;  Xaa Pos. 1,2,11,12
Seq#:10; Xaa Pos. 1,2,11,12
Seq#:11; Xaa Pos. 1,2,11,12
Seq#:12; Xaa Pos. 1,2,11,12
Seq#:13; Xaa Pos. 1,2,11,12
Seq#:14; Xaa Pos. 1,2,11,12
Seq#:15; Xaa Pos. 1,2,11,12
Seq#:16; Xaa Pos. 1,2,11,12
Seq#:17; Xaa Pos. 1,2,11,12
Seq#:18; Xaa Pos. 1,2,11,12
Seq#:19; Xaa Pos. 1,2,11,12
Seq#:20; Xaa Pos. 1,2,11,12
Seq#:21; Xaa Pos. 1,2,11,12
Seq#:22; Xaa Pos. 1,2,11,12
Seq#:23; Xaa Pos. 1,2,11,12
Seq#:24; Xaa Pos. 1,2,11,12
Seq#:25; Xaa Pos. 1,2,11,12
Seq#:26; Xaa Pos. 1,2,11,12
```

VERIFICATION SUMMARY   DATE: 10/30/2002
PATENT APPLICATION: US/10/086,814   TIME: 13:57:58

Input Set : A:\61010AB1.ST25.txt
Output Set: N:\CRF4\10302002\J086814.raw

```
L:214  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:261  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:314  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:373  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:426  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:485  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:544  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:597  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:656  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:721  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:780  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:845  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:898  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:945  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:998  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:1057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:1110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:1281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:1405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:1529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
```